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GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 28, 2002, 17:29:54 ; Search time 79.38 Seconds
(without alignments)
686.085 Million cell updates/sec

Title: US-09-502-984B-1

Perfect score: 1194

Sequence: 1 APPPNLDPDKFESKAALLA.....GGFWSAWSEPVSLTSDLD 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747981 seqs, 242050750 residues

Total number of hits satisfying chosen parameters: 747981

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pending_Patents_AA_New.* 1
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2: /cgns_6/ptodata/1/paa/US06_NEW_COMBO.pep:*
3: /cgns_6/ptodata/1/paa/US07_NEW_COMBO.pep:*
4: /cgns_6/ptodata/1/paa/US08_NEW_COMBO.pep:*
5: /cgns_6/ptodata/1/paa/US09_NEW_COMBO.pep:*
6: /cgns_6/ptodata/1/paa/US10_NEW_COMBO.pep:*
7: /cgns_6/ptodata/1/paa/US60_NEW_COMBO.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1194	100.0	225	5 US-09-502-984B-1
2	1194	100.0	508	5 US-09-502-984B-1
3	1177	98.6	228	5 US-09-791-537-9806
4	1185.5	97.0	227	5 US-09-791-537-98134
5	1133	94.9	215	5 US-09-791-537-105911
6	1123	94.1	213	5 US-09-791-537-67299
7	1112	93.1	211	5 US-09-502-984B-2
8	1112	93.1	211	5 US-09-791-537-85927
9	1100	92.1	211	5 US-09-502-984B-18
10	1099	92.0	211	5 US-09-502-984B-7
11	1097	91.9	211	5 US-09-502-984B-12
12	1096	91.8	211	5 US-09-502-984B-13
13	1096	91.8	211	5 US-09-502-984B-14
14	1096	91.8	211	5 US-09-502-984B-15
15	1095	91.7	211	5 US-09-502-984B-11
16	1091	91.4	211	5 US-09-502-984B-19
17	1090	91.3	211	5 US-09-502-984B-9
18	1090	91.3	211	5 US-09-502-984B-10
19	1088.5	91.2	212	5 US-09-502-984B-3
20	1086	91.0	211	5 US-09-502-984B-4
21	1086	91.0	211	5 US-09-502-984B-5
22	1086	91.0	211	5 US-09-502-984B-17
23	1086	91.0	211	5 US-09-502-984B-20
24	1083	90.7	211	5 US-09-502-984B-8
25	1080	90.5	211	5 US-09-502-984B-16
26	1077	90.2	211	5 US-09-502-984B-24
27	1077	90.2	211	5 US-09-502-984B-25
28	1076	90.1	211	5 US-09-502-984B-25
29	1074	89.9	211	5 US-09-502-984B-23
30	1072	89.8	211	5 US-09-502-984B-22
31	1072	89.8	211	5 US-09-502-984B-26
32	1071	89.7	211	5 US-09-502-984B-28
33	1061	88.9	211	5 US-09-502-984B-27
34	1060	88.8	211	5 US-09-502-984B-6
35	1060	88.8	249	5 US-09-502-984B-37
36	1049	87.9	211	5 US-09-502-984B-29
37	982.5	82.3	507	5 US-09-791-537-1440
38	982.5	82.3	507	5 US-09-791-537-12514
39	981.5	82.2	507	5 US-09-791-537-9845
40	966.5	80.9	265	5 US-09-791-537-4913
41	965.5	80.9	316	5 US-09-791-537-5613
42	851	71.3	229	5 US-09-791-537-40030
43	846	70.9	229	5 US-09-791-537-40031
44	222.5	18.5	17.5	5 US-09-831-158A-0055
45	205	17.2	625	6 US-09-099-895-34

ALIGNMENTS

RESULT	1	US-09-502-984B-1
OY	1	APPNPNLDPDKFESKAALLA.....GGFWSAWSEPVSLTSDLD 60
Db	1	DEPPNPLDPDKFESKAALLAARGPEELICFTERLEDLVCFWEEASAGVGPGNFSYQLE 60
OY	61	DEPWKLCLRHOAPTARGAVRFCSLPTADTSFVPLRYTAASGAPRHYRHINENVL 120
Db	61	DEPWKLCLRHOAPTARGAVRFCSLPTADTSFVPLRYTAASGAPRHYRHINENVL 120
OY	121	LDAPVGIVARIADESCHVVLWLPLPETPMTHIREVDVYDAGNGAGSVORVEILEGRTE 180
Db	121	LDAPVGIVARIADESCHVVLWLPLPETPMTHIREVDVYDAGNGAGSVORVEILEGRTE 180
OY	181	CYLSNLNRGRTTRYFAVRARMAEPSFGFGFWSAWSEPVSLTSDLD 225
Db	181	CYLSNLNRGRTTRYFAVRARMAEPSFGFGFWSAWSEPVSLTSDLD 225

RESULT 2
US-09-791-537-99806
; Sequence 99805, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 99806
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-791-537-99806

Query Match 100.0%; Score 1194; DB 5; Length 508;
Best Local Similarity 100.0%; Pred. No. 7.6e-106; Mismatches 0; Indels 0; Gaps 0;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPPNLDPKPFESKAALLAARGPPEELCFTTERLEDLVCFWEEASAGVGPGNFSYQLE 60

Db 25 APPPNLDPKPFESKAALLAARGPPEELCFTTERLEDLVCFWEEASAGVGPGNFSYQLE 84

Qy 61 DEPKWKLRLHQAPTARGAVRVCWSLTTADISSFPVPLRVTAASGAPRYHRVHINEVVL 120

Db 85 DEPKWKLRLHQAPTARGAVRVCWSLTTADISSFPVPLRVTAASGAPRYHRVHINEVVL 144

Qy 121 LDAPVGVLVARLADESGHVLRLMLPPPTPMISHIREVDVSAAGNGAGSVQRVEILEGRTE 180

Db 145 LDAPVGVLVARLADESGHVLRLMLPPPTPMISHIREVDVSAAGNGAGSVQRVEILEGRTE 204

Qy 181 CVLSNLRGRTRTFAVRMAEPSFSGFWASAWSEPVSLTSDLD 225

Db 205 CVLSNLRGRTRTFAVRMAEPSFSGFWASAWSEPVSLTSDLD 249

RESULT 3

US-09-791-537-38134

; Sequence 38134, Application US/09/791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 68105

; LENGTH: 227

; TYPE: PRT

; ORGANISM: pdb 1EERB

US-09-791-537-68105

Query Match 97.0%; Score 1158.5; DB 5; Length 227;

Best Local Similarity 98.2%; Pred. No. 6.7e-103; Mismatches 3; Indels 1; Gaps 1;

Matches 220; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 2 PPNLDPKPFESKAALLAARGPPEELCFTTERLEDLVCFWEEASAGVGPGNFSYQLE 61

Db 4 PPNLDPKPFESKAALLAARGPPEELCFTTERLEDLVCFWEEASAGVGPGNFSYQLE 62

Qy 62 EPWKLRLHQAPTARGAVRVCWSLTTADISSFPVPLRVTAASGAPRYHRVHINEVVL 121

Db 63 EPWKLRLHQAPTARGAVRVCWSLTTADISSFPVPLRVTAASGAPRYHRVHINEVVL 122

Qy 122 DAPVGVLVARLADESGHVLRLMLPPPTPMISHIREVDVSAAGNGAGSVQRVEILEGRTE 181

Db 123 DAPVGVLVARLADESGHVLRLMLPPPTPMISHIREVDVSAAGNGAGSVQRVEILEGRTE 182

Qy 182 VLSNLRGRTRTFAVRMAEPSFSGFWASANSEPVSLTSDLD 225

Db 183 VLSNLRGRTRTFAVRMAEPSFSGFWASANSEPVSLTSDLD 226

RESULT 5

US-09-791-537-105911

; Sequence 105911, Application US/09/791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 105911

; LENGTH: 215

; TYPE: PRT

; ORGANISM: pdb 1EBA

US-09-791-537-105911

Query Match 98.6%; Score 1177; DB 5; Length 228;

Best Local Similarity 98.7%; Pred. No. 1.1e-104; Mismatches 0; Indels 0; Gaps 0;

Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APPPNLDPKPFESKAALLAARGPPEELCFTTERLEDLVCFWEEASAGVGPGNFSYQLE 60

Db 4 APPPNLDPKPFESKAALLAARGPPEELCFTTERLEDLVCFWEEASAGVGPGNFSYQLE 63

Qy 61 DEPKWKLRLHQAPTARGAVRVCWSLTTADISSFPVPLRVTAASGAPRYHRVHINEVVL 120

Db 64 DEPKWKLRLHQAPTARGAVRVCWSLTTADISSFPVPLRVTAASGAPRYHRVHINEVVL 123

Qy 121 LDAPVGVLVARLADESGHVLRLMLPPPTPMISHIREVDVSAAGNGAGSVQRVEILEGRTE 180

Db 124 LDAPVGVLVARLADESGHVLRLMLPPPTPMISHIREVDVSAAGNGAGSVQRVEILEGRTE 183

Query Match 94.9%; Score 1133; DB 5; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.7e-100; Mismatches 0; Indels 0; Gaps 0;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KFESKAALLAARGPPEELCFTTERLEDLVCFWEEASAGVGPGNFSYQLEDEPKWKLRL 69

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Db 1 KFESKAALLARGPPEELICFTERILEDVCFWEEASAGVGPGNFSYQLEDEPWKLCR 60
; SEQ ID NO 2
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-502-984B-2

Qy 70 HQAPTAGVRFWCSLTADTSFVPLERLRTVAASGAPRYHRVHINEVVLDAPIGLA 129
Db 61 HQAPTAGVRFWCSLTADTSFVPLERLRTVAASGAPRYHRVHINEVVLDAPIGLA 120

Qy 130 RLADESCHVVLWLPPETPMSHIREDVSGNGAGSVORVELLEGTECVLSNLRGR 189
Db 121 RLADESCHVVLWLPPETPMSHIREDVSGNGAGSVORVELLEGTECVLSNLRGR 180

Qy 181 TRYFAVRARMAEPSFGFWSAWSEPVSLITPSDL 215
Db 181 TRYFAVRARMAEPSFGFWSAWSEPVSLITPSDL 215

RESULT 6
US-09-791-537-67299
; Sequence 67299, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SEQ ID NO 67299
; TYPE: PRT
; ORGANISM: pdb 1ERNA
; US-09-791-537-67299

Query Match 93.1%; Score 1112; DB 5; Length 211;
Best Local Similarity 100.0%; Pred. No. 1. 7e-98;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 67299

RESULT 8
US-09-791-537-86927
; Sequence 86927, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 86927
; LENGTH: 211
; TYPE: PRT
; ORGANISM: pdb 1EBPA
; US-09-791-537-86927

Query Match 93.1%; Score 1112; DB 5; Length 211;
Best Local Similarity 100.0%; Pred. No. 1. 7e-98;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 86927

RESULT 7
US-09-502-984B-2
; Sequence 2, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502, 984B
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/120, 009
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/131, 674
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1

Query Match 93.1%; Score 1112; DB 5; Length 211;
Best Local Similarity 100.0%; Pred. No. 1. 7e-98;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
FILE REFERENCE: A-68126-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/502, 984B
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/120, 009
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131, 674
PRIOR FILING DATE: 1999-04-29
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1

RESULT 9
US-09-502-984B-18
; Sequence 18, Application US/09502984B

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; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RFM/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY FILING DATE: 1999-02-11
; PRIORITY APPLICATION NUMBER: 60/131,674
; PRIORITY FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; US-09-502-984B-18

Query Match 92.1%; Score 1100; DB 5; Length 211;
Best Local Similarity 99.1%; Pred. No. 2. 4e-97; 0; Mismatches 2; Indels 0; Gaps 0;
Matches 209; Conservative 0;

Qy 10 KFESKAALLAARGPEELICFFTERLEDLVCFNEEAASAGVGPGNNSFSYQLEDEPWKLCR 69
Db 1 KFESKAALLAARGPEELICFFTERLEDLVCFNEEAASAGVGPGNNSFSYQLEDEPWKLCR 60

Qy 70 HOAPTARGAVREWCSLPTADTSSFVPLRVTAAASGAPRYHRVHINEVVLIDAPVGLVA 129
Db 61 HOAPTARGAVREWCSLPTADTSSFVPLRVTAAASGAPRYHRVHINEVVLIDAPVGLVA 120

Qy 130 RLADESHVVLWLPETPMTHIRYEVDSAGNGAGSVOVLELEGRCVLSNLGR 189
Db 121 RLADESHVVLWLPETPMTHIRYEVDSAGNGAGSVOVLELEGRCVLSNLGR 180

Qy 190 TRYFAVRAMAEPSPFGFWAWSEPVSLT 220
Db 181 TRYFAVRAMAEPSPFGFWAWSEPVSLT 211

RESULT 11
US-09-502-984B-12
; Sequence 12, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RFM/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY FILING DATE: 1999-02-11
; PRIORITY APPLICATION NUMBER: 60/131,674
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; US-09-502-984B-12

Query Match 91.9%; Score 1097; DB 5; Length 211;
Best Local Similarity 97.6%; Pred. No. 4. 7e-97; 5; Mismatches 0; Indels 0; Gaps 0;
Matches 206; Conservative 5;

Qy 10 KFESKAALLAARGPEELICFFTERLEDLVCFNEEAASAGVGPGNNSFSYQLEDEPWKLCR 69
Db 1 KFESKAALLAARGPEELICFFTERLEDLVCFNEEAASAGVGPGNNSFSYQLEDEPWKLCR 60

Qy 70 HOAPTARGAVREWCSLPTADTSSFVPLRVTAAASGAPRYHRVHINEVVLIDAPVGLVA 129
Db 61 HOAPTARGAVREWCSLPTADTSSFVPLRVTAAASGAPRYHRVHINEVVLIDAPVGLVA 120

Qy 130 RLADESHVVLWLPETPMTHIRYEVDSAGNGAGSVOVLELEGRCVLSNLGR 189
Db 121 RLADESHVVLWLPETPMTHIRYEVDSAGNGAGSVOVLELEGRCVLSNLGR 180

Qy 190 TRYFAVRAMAEPSPFGFWAWSEPVSLT 220
Db 181 TRYFAVRAMAEPSPFGFWAWSEPVSLT 211

RESULT 12
US-09-502-984B-13
; Sequence 13, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RFM/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY FILING DATE: 1999-02-11
; PRIORITY APPLICATION NUMBER: 60/131,674
; PRIORITY FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37

Query Match 92.0%; Score 1099; DB 5; Length 211;
Best Local Similarity 98.1%; Pred. No. 3e-97; 4; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KFESKAALLAARGPEELICFFTERLEDLVCFNEEAASAGVGPGNNSFSYQLEDEPWKLCR 69
Db 1 KFESKAALLAARGPEELICFFTERLEDLVCFNEEAASAGVGPGNNSFSYQLEDEPWKLCR 60

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 211
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984B-13

Query Match 91.8%; Score 1096; DB 5; Length 211;
Best Local Similarity 97.6%; Pred. No. 5.9e-97; Mismatches 0; Indels 0; Gaps 0;
Matches 206; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 10 KFESKALLAARGPEELICCFTERLEDLVCWEAASAGVGPGNYFSYQLEDEPWKLCRL 69
Db 1 KFESKALLAARGPEELICCFTERLEDLVCWEAASAGVGPGNYFSYQLEDEPWKLCRL 60

QY 70 HOAPTAGVAREWCSLPTADSSFVPLERLTAAAGPAPHRVHINEVWLLDAPGLVA 129
Db 61 HOAPTAGVAREWCSLPTADSSFVPLERLTAAAGPAPHRVHINEVWLLDAPGLVA 120

QY 130 RLADESCHVWLRLPPETPMPSHIRVEVDYSAAGNGAGSVORVELLEGRCVLSNLRGR 189
Db 121 RLADESCHVWLRLPPETPMPSHIRVEVDYSAAGNGAGSVORVELLEGRCVLSNLRGR 180

QY 190 TRYFAVRARMAEPSFGFWSAWSEPVSLT 220
Db 181 TRYFAVRARMAEPSFGFWSAWSEPVSLT 211

RESULT 13
US-09-502-984B-14

; Sequence 14, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RET/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502, 984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY NUMBER: 60/131, 674
; PRIORITY NUMBER: 60/120, 009
; PRIORITY NUMBER: 60/131, 674
; PRIORITY FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 211
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984B-15

Query Match 91.8%; Score 1096; DB 5; Length 211;
Best Local Similarity 97.6%; Pred. No. 5.9e-97; Mismatches 0; Indels 0; Gaps 0;
Matches 206; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 10 KFESKALLAARGPEELICCFTERLEDLVCWEAASAGVGPGNYFSYQLEDEPWKLCRL 69
Db 1 KFESKALLAARGPEELICCFTERLEDLVCWEAASAGVGPGNYFSYQLEDEPWKLCRL 60

QY 70 HOAPTAGVAREWCSLPTADSSFVPLERLTAAAGPAPHRVHINEVWLLDAPGLVA 129
Db 61 HOAPTAGVAREWCSLPTADSSFVPLERLTAAAGPAPHRVHINEVWLLDAPGLVA 120

QY 130 RLADESCHVWLRLPPETPMPSHIRVEVDYSAAGNGAGSVORVELLEGRCVLSNLRGR 189
Db 121 RLADESCHVWLRLPPETPMPSHIRVEVDYSAAGNGAGSVORVELLEGRCVLSNLRGR 180

QY 190 TRYFAVRARMAEPSFGFWSAWSEPVSLT 220
Db 181 TRYFAVRARMAEPSFGFWSAWSEPVSLT 211

RESULT 15
US-09-502-984B-11

; Sequence 11, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RET/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502, 984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY NUMBER: 60/120, 009
; PRIORITY FILING DATE: 1999-02-11
; PRIORITY NUMBER: 60/131, 674
; PRIORITY FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 211
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-502-984B-11

Query Match 91.8%; Score 1096; DB 5; Length 211;
Best Local Similarity 97.8%; Pred. No. 5.9e-97; Mismatches 0; Indels 0; Gaps 0;
Matches 206; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 10 KFESKALLAARGPEELICCFTERLEDLVCWEAASAGVGPGNYFSYQLEDEPWKLCRL 69
Db 1 KFESKALLAARGPEELICCFTERLEDLVCWEAASAGVGPGNYFSYQLEDEPWKLCRL 60

QY 70 HOAPTAGVAREWCSLPTADSSFVPLERLTAAAGPAPHRVHINEVWLLDAPGLVA 129
Db 61 HOAPTAGVAREWCSLPTADSSFVPLERLTAAAGPAPHRVHINEVWLLDAPGLVA 120

QY 130 RLADESCHVWLRLPPETPMPSHIRVEVDYSAAGNGAGSVORVELLEGRCVLSNLRGR 189
Db 121 RLADESCHVWLRLPPETPMPSHIRVEVDYSAAGNGAGSVORVELLEGRCVLSNLRGR 180

QY 190 TRYFAVRARMAEPSFGFWSAWSEPVSLT 220
Db 190 TRYFAVRARMAEPSFGFWSAWSEPVSLT 220

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Best Local Similarity 97.6%; Pred. No. 7.4e-97; Matches 206; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy 10 KFSSKAALLAARGPPEELICFTERLEDIVCFWIERASAGVGPGNYSFYQLEDEPWKICRL 69
Db 1 KFSSKAALLAARGPPEELICFTERLEDIVCFWIERASAGVGPGNYSFYQLEDEPWKICRL 60
Qy 70 HQPTARGAVRWCSLPTADISFVPLERVTRASGAPRYHRVHINEVVLIDAPVGLVA 129
Db 61 HQPTARGAVRWCSLPTADISFVPLERVTRASGAPRYHRVHINEVVLIDAPVGLVA 120
Qy 130 RLADESGIVVLRULPPPTPMTHIRVEDVSAAGNGAGSVORVEILRGRTECVLSNLRGR 189
Db 121 RLADESGIVVLRULPPPTPMTHIRVEIDISAGNGAGSVQRVEILRGRTECVLSNLRGR 180
Qy 190 TRYTFAYVARMAPSFEGFWASSEPVSLIT 220
Db 181 TRYTFAYVARMAPSFEGFWASSEPVSLIT 211

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Search completed: August 28, 2002, 17:39:04
 Job time: 550 sec